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><MW: 120922
MVFPMWTLKRQILILFNIILISKLLGARWFPKTLPCDVTLDVPKNHVIVDCTDKHLTEIP
GGIPTNTTNLTLTINHIPDISPASFHRLDHLVEIDFRCNCVPIPLGSKNNMCIKRLQIKP
RSFSGLTYLKSLYLDGNQLLEIPQGLPPSLQLLSLEANNIFSIRKENLTELANIEILYLG
QNCYYRNPCYVSYSIEKDAFLNLTKLKVLSLKDNNVTAVPTVLPSTLTELYLYNNMIAKI
QEDDFNNLNQLQILDLSGNCPRCYNAPFPCAPCKNNSPLQIPVNAFDALTELKVLRLHSN
SLQHVPPRWFKNINKLQELDLSQNFLAKEIGDAKFLHFLPSLIQLDLSFNFELQVYRASM
NLSQAFSSLKSLKILRIRGYVFKELKSFNLSPLHNLQNLEVLDLGTNFIKIANLSMFKQF
KRLKVIDLSVNKISPSGDSSEVGFCSNARTSVESYEPQVLEQLHYFRYDKYARSCRFKNK
EASFMSVNESCYKYGQTLDLSKNSIFFVKSSDFQHLSFLKCLNLSGNLISQTLNGSEFQP
LAELRYLDFSNNRLDLLHSTAFEELHKLEVLDISSNSHYFQSEGITHMLNFTKNLKVLQK
LMMNDNDISSSTSRTMESESLRTLEFRGNHLDVLWREGDNRYLQLFKNLLKLEELDISKN
SLSFLPSGVFDGMPPNLKNLSLAKNGLKSFSWKKLQCLKNLETLDLSHNQLTTVPERLSN
CSRSLKNLILKNNQIRSLTKYFLQDAFQLRYLDLSSNKIQMIQKTSFPENVLNNLKMLLL
HHNRFLCTCDAVWFVWWVNHTEVTIPYLATDVTCVGPGAHKGQSVISLDLYTCELDLTNL
ILFSLSISVSLFLMVMMTASHLYFWDVWYIYHFCKAKIKGYQRLISPDCCYDAFIVYDTK
DPAVTEWVLAELVAKLEDPREKHFNLCLEERDWLPGQPVLENLSQSIQLSKKTVFVMTDK
YAKTENFKIAFYLSHQRLMDEKVDVIILIFLEKPFQKSKFLQLRKRLCGSSVLEWPTNPQ
AHPYFWQCLKNALATDNHVAYSQVFKETV
```

FIG. 1

```
><insert starts here>CCCATCTCAAGCTGATCTTGGCACCTCTCATGCTCTGCTCTCTTCAACCAGACCTCTACA
TTCCATTTTGGAAGAAGACTAAAA
><MET {trans=1-s, dir=f, res=1}>
ATGGTGTTTCCAATGTGGACACTGAAGAGACAAATTCTTATCCTTTTTAACATAATCCTA
ATTTCCAAACTCCTTGGGGCTAGATGGTTTCCTAAAACTCTGCCCTGTGATGTCACTCTG
GATGTTCCAAAGAACCATGTGATCGTGGACTGCACAGACAAGCATTTGACAGAAATTCCT
GGAGGTATTCCCACGAACACCACGAACCTCACCCTCACCATTAACCACATACCAGACATC
TCCCCAGCGTCCTTTCACAGACTGGACCATCTGGTAGAGATCGATTTCAGATGCAACTGT
GTACCTATTCCACTGGGGTCAAAAAACAACATGTGCATCAAGAGGCTGCAGATTAAACCC
AGAAGCTTTAGTGGACTCACTTATTTAAAATCCCTTTACCTGGATGGAAACCAGCTACTA
GAGATACCGCAGGGCCTCCCGCCTAGCTTACAGCTTCTCAGCCTTGAGGCCAACAACATC
TTTTCCATCAGAAAAGAGAATCTAACAGAACTGGCCAACATAGAAATACTCTACCTGGGC
CAAAACTGTTATTATCGAAATCCTTGTTATGTTTCATATTCAATAGAGAAAGATGCCTTC
CTAAACTTGACAAAGTTAAAAGTGCTCTCCCTGAAAGATAACAATGTCACAGCCGTCCCT
ACTGTTTTGCCATCTACTTTAACAGAACTATATCTCTACAACAACATGATTGCAAAAATC
CAAGAAGATGATTTTAATAACCTCAACCAATTACAAATTCTTGACCTAAGTGGAAATTGC
CCTCGTTGTTATAATGCCCCATTTCCTTGTGCGCCGTGTAAAAATAATTCTCCCCTACAG
ATCCCTGTAAATGCTTTTGATGCGCTGACAGAATTAAAAGTTTTACGTCTACACAGTAAC
TCTCTTCAGCATGTGCCCCCAAGATGGTTTAAGAACATCAACAAACTCCAGGAACTGGAT
CTGTCCCAAAACTTCTTGGCCAAAGAAATTGGGGATGCTAAATTTCTGCATTTTCTCCCC
AGCCTCATCCAATTGGATCTGTCTTTCAATTTTGAACTTCAGGTCTATCGTGCATCTATG
AATCTATCACAAGCATTTTCTTCACTGAAAAGCCTGAAAATTCTGCGGATCAGAGGATAT
GTCTTTAAAGAGTTGAAAAGCTTTAACCTCTCGCCATTACATAATCTTCAAAATCTTGAA
GTTCTTGATCTTGGCACTAACTTTATAAAAATTGCTAACCTCAGCATGTTTAAACAATTT
AAAAGACTGAAAGTCATAGATCTTTCAGTGAATAAAATATCACCTTCAGGAGATTCAAGT
GAAGTTGGCTTCTGCTCAAATGCCAGAACTTCTGTAGAAAGTTATGAACCCCAGGTCCTG
GAACAATTACATTATTTCAGATATGATAAGTATGCAAGGAGTTGCAGATTCAAAAACAAA
GAGGCTTCTTTCATGTCTGTTAATGAAAGCTGCTACAAGTATGGGCAGACCTTGGATCTA
AGTAAAAATAGTATATTTTTTGTCAAGTCCTCTGATTTTCAGCATCTTTCTTTCCTCAAA
```

FIG. 2A

```
TGCCTGAATCTGTCAGGAAATCTCATTAGCCAAACTCTTAATGGCAGTGAATTCCAACCT
TTAGCAGAGCTGAGATATTTGGACTTCTCCAACAACCGGCTTGATTTACTCCATTCAACA
GCATTTGAAGAGCTTCACAAACTGGAAGTTCTGGATATAAGCAGTAATAGCCATTATTTT
CAATCAGAAGGAATTACTCATATGCTAAACTTTACCAAGAACCTAAAGGTTCTGCAGAAA
CTGATGATGAACGACAATGACATCTCTTCCTCCACCAGCAGGACCATGGAGAGTGAGTCT
CTTAGAACTCTGGAATTCAGAGGAAATCACTTAGATGTTTTATGGAGAGAAGGTGATAAC
AGATACTTACAATTATTCAAGAATCTGCTAAAATTAGAGGAATTAGACATCTCTAAAAAT
TCCCTAAGTTTCTTGCCTTCTGGAGTTTTTGATGGTATGCCTCCAAATCTAAAGAATCTC
TCTTTGGCCAAAAATGGGCTCAAATCTTTCAGTTGGAAGAAACTCCAGTGTCTAAAGAAC
CTGGAAACTTTGGACCTCAGCCACAACCAACTGACCACTGTCCCTGAGAGATTATCCAAC
TGTTCCAGAAGCCTCAAGAATCTGATTCTTAAGAATAATCAAATCAGGAGTCTGACGAAG
TATTTTCTACAAGATGCCTTCCAGTTGCGATATCTGGATCTCAGCTCAAATAAAATCCAG
ATGATCCAAAAGACCAGCTTCCCAGAAAATGTCCTCAACAATCTGAAGATGTTGCTTTTG
CATCATAATCGGTTTCTGTGCACCTGTGATGCTGTGTGGTTTGTCTGGTGGGTTAACCAT
ACGGAGGTGACTATTCCTTACCTGGCCACAGATGTGACTTGTGTGGGGCCAGGAGCACAC
AAGGGCCAAAGTGTGATCTCCCTGGATCTGTACACCTGTGAGTTAGATCTGACTAACCTG
ATTCTGTTCTCACTTTCCATATCTGTATCTCTCTTTCTCATGGTGATGATGACAGCAAGT
CACCTCTATTTCTGGGATGTGTGGTATATTTACCATTTCTGTAAGGCCAAGATAAAGGGG
TATCAGCGTCTAATATCACCAGACTGTTGCTATGATGCTTTTATTGTGTATGACACTAAA
GACCCAGCTGTGACCGAGTGGGTTTTGGCTGAGCTGGTGGCCAAACTGGAAGACCCAAGA
GAGAAACATTTTAATTTATGTCTCGAGGAAAGGGACTGGTTACCAGGGCAGCCAGTTCTG
GAAAACCTTTCCCAGAGCATACAGCTTAGCAAAAAGACAGTGTTTGTGATGACAGACAAG
TATGCAAAGACTGAAAATTTTAAGATAGCATTTTACTTGTCCCATCAGAGGCTCATGGAT
GAAAAAGTTGATGTGATTATCTTGATATTTCTTGAGAAGCCCTTTCAGAAGTCCAAGTTC
CTCCAGCTCCGGAAAAGGCTCTGTGGGAGTTCTGTCCTTGAGTGGCCAACAAACCCGCAA
GCTCACCCATACTTCTGGCAGTGTCTAAAGAACGCCCTGGCCACAGACAATCATGTGGCC
TATAGTCAGGTGTTCAAGGAAACGGTCTAGCCCTTCTTTGCAAAACACAACTGCCTAGTT
TACCAAGGAGAGGCCTGGC
```

FIG. 2B

```
MENMFLQSSMLTCIFLLISGSCELCAEENFSRSYPCDEKKQNDSVIAECSNRRLQEVPQT
VGKYVTELDLSDNFITHITNESFQGLQNLTKINLNHNPNVQHQNGNPGIQSNGLNITDGA
FLNLKNLRELLLEDNQLPQIPSGLPESLTELSLIQNNIYNITKEGISRLINLKNLYLAWN
CYFNKVCEKTNIEDGVFETLTNLELLSLSFNSLSHVPPKLPSSLRKLFLSNTQIKYISEE
DFKGLINLTLLDLSGNCPRCFNAPFPCVPCDGGASINIDRFAFQNLTQLRYLNLSSTSLR
KINAAWFKNMPHLKVLDLEFNYLVGEIVSGAFLTMLPRLEILDLSFNYIKGSYPQHINIS
RNFSKLLSLRALHLRGYVFQELREDDFQPLMQLPNLSTINLGINFIKQIDFKLFQNFSNL
EIIYLSENRISPLVKDTRQSYANSSSFQRHIRKRRSTDFEFDPHSNFYHFTRPLIKPQCA
AYGKALDLSLNSIFFIGPNQFENLPDIACLNLSANSNAQVLSGTEFSAIPHVKYLDLTNN
RLDFDNASALTELSDLEVLDLSYNSHYFRIAGVTHHLEFIQNFTNLKVLNLSHNNIYTLT
DKYNLESKSLVELVFSGNRLDILWNDDDNRYISIFKGLKNLTRLDLSLNRLKHIPNEAFL
NLPASLTELHINDNMLKFFNWTLLQQFPRLELLDLRGNKLLFLTDSLSDFTSSLRTLLLS
HNRISHLPSGFLSEVSSLKHLDLSSNLLKTINKSALETKTTTKLSMLELHGNPFECTCDI
GDFRRWMDEHLNVKIPRLVDVICASPGDQRGKSIVSLELTTCVSDVTAVILFFFTFFITT
MVMLAALAHHLFYWDVWFIYNVCLAKVKGYRSLSTSQTFYDAYISYDTKDASVTDWVINE
LRYHLEESRDKNVLLCLEERDWDPGLAIIDNLMQSINQSKKTVFVLTKKYAKSWNFKTAF
YLALQRLMDENMDVIIFILLEPVLQHSQYLRLRQRICKSSILQWPDNPKAEGLFWQTLRN
VVLTENDSRYNNMYVDSIKQY


<1041 residues, 0 stop; molecular weight: 119856.26
```

FIG. 3

```
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AAC
><MET {trans=1-s, dir=f, res=1}>
ATGGAAAACATGTTCCTTCAGTCGTCAATGCTGACCTGCATTTTCCTGCTAATATCTGGT
TCCTGTGAGTTATGCGCCGAAGAAAATTTTTCTAGAAGCTATCCTTGTGATGAGAAAAAG
CAAAATGACTCAGTTATTGCAGAGTGCAGCAATCGTCGACTACAGGAAGTTCCCCAAACG
GTGGGCAAATATGTGACAGAACTAGACCTGTCTGATAATTTCATCACACACATAACGAAT
GAATCATTTCAAGGGCTGCAAAATCTCACTAAAATAAATCTAAACCACAACCCCAATGTA
CAGCACCAGAACGGAAATCCCGGTATACAATCAAATGGCTTGAATATCACAGACGGGGCA
TTCCTCAACCTAAAAAACCTAAGGGAGTTACTGCTTGAAGACAACCAGTTACCCCAAATA
CCCTCTGGTTTGCCAGAGTCTTTGACAGAACTTAGTCTAATTCAAAACAATATATACAAC
ATAACTAAAGAGGGCATTTCAAGACTTATAAACTTGAAAAATCTCTATTTGGCCTGGAAC
TGCTATTTTAACAAAGTTTGCGAGAAAACTAACATAGAAGATGGAGTATTTGAAACGCTG
ACAAATTTGGAGTTGCTATCACTATCTTTCAATTCTCTTTCACACGTGCCACCCAAACTG
CCAAGCTCCCTACGCAAACTTTTTCTGAGCAACACCCAGATCAAATACATTAGTGAAGAA
GATTTCAAGGGATTGATAAATTTAACATTACTAGATTTAAGCGGGAACTGTCCGAGGTGC
TTCAATGCCCCATTTCCATGCGTGCCTTGTGATGGTGGTGCTTCAATTAATATAGATCGT
TTTGCTTTTCAAAACTTGACCCAACTTCGATACCTAAACCTCTCTAGCACTTCCCTCAGG
AAGATTAATGCTGCCTGGTTTAAAAATATGCCTCATCTGAAGGTGCTGGATCTTGAATTC
AACTATTTAGTGGGAGAAATAGTCTCTGGGGCATTTTTAACGATGCTGCCCCGCTTAGAA
ATACTTGACTTGTCTTTTAACTATATAAAGGGGAGTTATCCACAGCATATTAATATTTCC
AGAAACTTCTCTAAACTTTTGTCTCTACGGGCATTGCATTTAAGAGGTTATGTGTTCCAG
GAACTCAGAGAAGATGATTTCCAGCCCCTGATGCAGCTTCCAAACTTATCGACTATCAAC
TTGGGTATTAATTTTATTAAGCAAATCGATTTCAAACTTTTCCAAAATTTCTCCAATCTG
```

FIG. 4A

GAAATTATTTACTTGTCAGAAAACAGAATATCACCGTTGGTAAAAGATACCCGGCAGAGT
TATGCAAATAGTTCCTCTTTTCAACGTCATATCCGGAAACGACGCTCAACAGATTTTGAG
TTTGACCCACATTCGAACTTTTATCATTTCACCCGTCCTTTAATAAAGCCACAATGTGCT
GCTTATGGAAAAGCCTTAGATTTAAGCCTCAACAGTATTTTCTTCATTGGGCCAAACCAA
TTTGAAAATCTTCCTGACATTGCCTGTTTAAATCTGTCTGCAAATAGCAATGCTCAAGTG
TTAAGTGGAACTGAATTTTCAGCCATTCCTCATGTCAAATATTTGGATTTGACAAACAAT
AGACTAGACTTTGATAATGCTAGTGCTCTTACTGAATTGTCCGACTTGGAAGTTCTAGAT
CTCAGCTATAATTCACACTATTTCAGAATAGCAGGCGTAACACATCATCTAGAATTTATT
CAAAATTTCACAAATCTAAAAGTTTTAAACTTGAGCCACAACAACATTTATACTTTAACA
GATAAGTATAACCTGGAAAGCAAGTCCCTGGTAGAATTAGTTTTCAGTGGCAATCGCCTT
GACATTTTGTGGAATGATGATGACAACAGGTATATCTCCATTTTCAAAGGTCTCAAGAAT
CTGACACGTCTGGATTTATCCCTTAATAGGCTGAAGCACATCCCAAATGAAGCATTCCTT
AATTTGCCAGCGAGTCTCACTGAACTACATATAAATGATAATATGTTAAAGTTTTTTAAC
TGGACATTACTCCAGCAGTTTCCTCGTCTCGAGTTGCTTGACTTACGTGGAAACAAACTA
CTCTTTTTAACTGATAGCCTATCTGACTTTACATCTTCCCTTCGGACACTGCTGCTGAGT
CATAACAGGATTTCCCACCTACCCTCTGGCTTTCTTTCTGAAGTCAGTAGTCTGAAGCAC
CTCGATTTAAGTTCCAATCTGCTAAAAACAATCAACAAATCCGCACTTGAAACTAAGACC
ACCACCAAATTATCTATGTTGGAACTACACGGAAACCCCTTTGAATGCACCTGTGACATT
GGAGATTTCCGAAGATGGATGGATGAACATCTGAATGTCAAAATTCCCAGACTGGTAGAT
GTCATTTGTGCCAGTCCTGGGGATCAAAGAGGGAAGAGTATTGTGAGTCTGGAGCTAACA
ACTTGTGTTTCAGATGTCACTGCAGTGATATTATTTTTCTTCACGTTCTTTATCACCACC
ATGGTTATGTTGGCTGCCCTGGCTCACCATTTGTTTTACTGGGATGTTTGGTTTATATAT
AATGTGTGTTTAGCTAAGGTAAAAGGCTACAGGTCTCTTTCCACATCCCAAACTTTCTAT
GATGCTTACATTTCTTATGACACCAAAGATGCCTCTGTTACTGACTGGGTGATAAATGAG

FIG. 4B

Sequence ss.DNA42663

```
CTGCGCTACCACCTTGAAGAGAGCCGAGACAAAAACGTTCTCCTTTGTCTAGAGGAGAGG
GATTGGGACCCGGGATTGGCCATCATCGACAACCTCATGCAGAGCATCAACCAAAGCAAG
AAAACAGTATTTGTTTTAACCAAAAAATATGCAAAAAGCTGGAACTTTAAAACAGCTTTT
TACTTGGCTTTGCAGAGGCTAATGGATGAGAACATGGATGTGATTATATTTATCCTGCTG
GAGCCAGTGTTACAGCATTCTCAGTATTTGAGGCTACGGCAGCGGATCTGTAAGAGCTCC
ATCCTCCAGTGGCCTGACAACCCGAAGGCAGAAGGCTTGTTTTGGCAAACTCTGAGAAAT
GTGGTCTTGACTGAAAATGATTCACGGTATAACAATATGTATGTCGATTCCATTAAGCAA
TACTAACTGACGTTAAGTCATGATTTCGCGCCATAATAAAGATGCAAAGGAATGACATTT
CTGTATTAGTTATCTATTGCTATGTAACAAATTATCCCAAAACTTAGTGGTTTAAAACAA
CACATTTGCTGGCCCACAGTTTTTGAGGGTCAGGAGTCCAGGCCCAGCATAACTGGGTCC
TCTGCTCAGGGTGTCTCAGAGGCTGCAATGTAGGTGTTCACCAGAGACATAGGCATCACT
GGGGTCACACTCATGTGGTTGTTTTCTGGATTCAATTCCTCCTGGGCTATTGGCCAAAGG
CTATACTCATGTAAGCCATGCGAGCCTCTCCCACAAGGCAGCTTGCTTCATCAGAGCTAG
CAAAAAAGAGAGGTTGCTAGCAAGATGAAGTCACAATCTTTTGTAATCGAATCAAAAAAG
TGATATCTCATCACTTTGGCCATATTCTATTTGTTAGAAGTAAACCACAGGTCCCACCAG
CTCCATGGGAGTGACCACCTCAGTCCAGGGAAAACAGCTGAAGACCAAGATGGTGAGCTC
TGATTGCTTCAGTTGGTCATCAACTATTTTCCCTTGACTGCTGTCCTGGGATGGCCTGCT
ATCTTGATGATAGATTGTGAATATCAGGAGGCAGGGATCACTGTGGACCATCTTAGCAGT
TGACCTAACACATCTTCTTTTCAATATCTAAGAACTTTTGCCACTGTGACTAATGGTCCT
AATATTAAGCTGTTGTTTATATTTATCATATATCTATGGCTACATGGTTATATTATGCTG
TGGTTGCGTTCGGTTTTATTTACAGTTGCTTTTACAAATATTTGCTGTAACATTTGACTT
CTAAGGTTTAGATGCCATTTAAGAACTGAGATGGATAGCTTTTAAAGCATCTTTTACTTC
TTACCATTTTTTAAAAGTATGCAGCTAAATTCGAAGCTTTTGGTCTATATTGTTAATTGC
CATTGCTGTAAATCTTAAAATGAATGAATAAAAATGTTTCATTTTACAAAAAAAAAAAAA
AAA
```

FIG. 4C

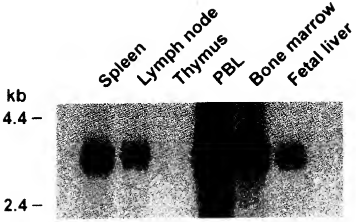

Spleen
Lymph node
Thymus
PBL
Bone marrow
Fetal liver
kb
4.4 –
2.4 –

FIG. 5A

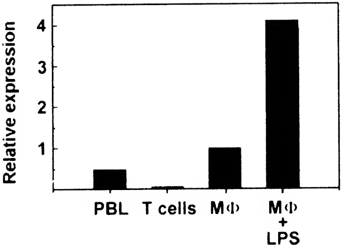

Relative expression
4
3
2
1
PBL
T cells
MΦ
MΦ + LPS

FIG. 5B

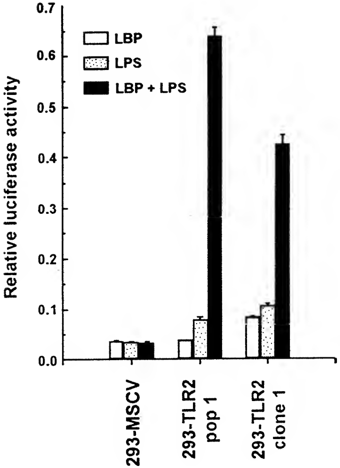

Relative luciferase activity
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
LBP
LPS
LBP + LPS
293-MSCV
293-TLR2 pop 1
293-TLR2 clone 1

FIG. 6A

FIG. 6B

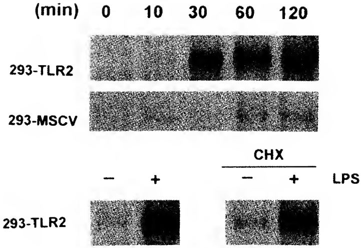


FIG. 6C

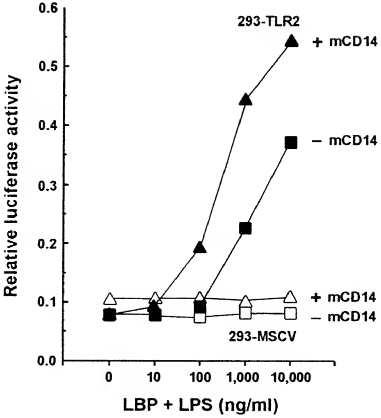

Relative luciferase activity
0.6
0.5
0.4
0.3
0.2
0.1
0.0
293-TLR2
+ mCD14
− mCD14
+ mCD14
− mCD14
293-MSCV
0
10
100
1,000
10,000
LBP + LPS (ng/ml)

FIG. 6D

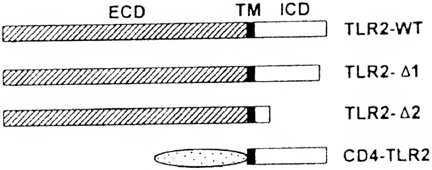

ECD
TM
ICD
TLR2-WT
TLR2- Δ1
TLR2- Δ2
CD4-TLR2

FIG. 7A

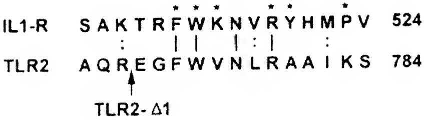
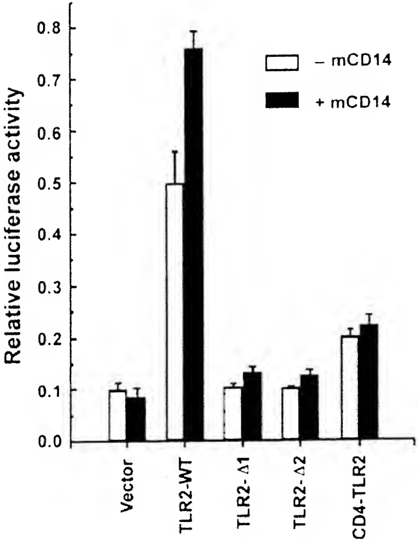
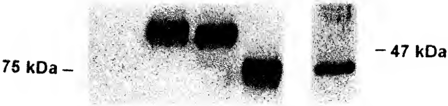

IL1-R
S A K T R F W K N V R Y H M P V 524
TLR2
A Q R E G F W V N L R A A I K S 784
TLR2- Δ1

FIG. 7B



Relative luciferase activity
0.0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
0.8
– mCD14
+ mCD14
Vector
TLR2-WT
TLR2- Δ1
TLR2- Δ2
CD4-TLR2

FIG. 7C



75 kDa –
– 47 kDa

FIG. 7D

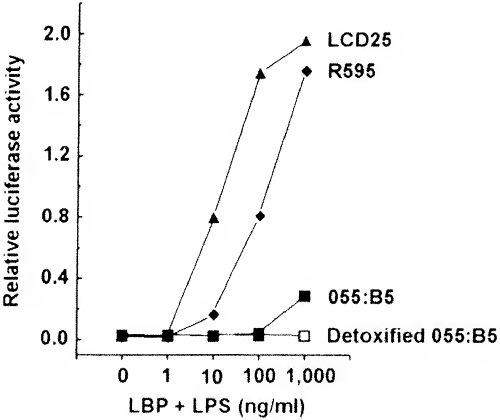

2.0
1.6
1.2
0.8
0.4
0.0
Relative luciferase activity
0
1
10
100
1,000
LBP + LPS (ng/ml)
LCD25
R595
055:B5
Detoxified 055:B5

FIG. 8A

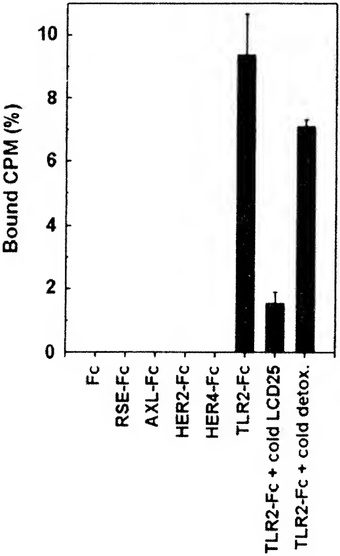

Bound CPM (%)
0
2
4
6
8
10
Fc
RSE-Fc
AXL-Fc
HER2-Fc
HER4-Fc
TLR2-Fc
TLR2-Fc + cold LCD25
TLR2-Fc + cold detox.

FIG. 8B

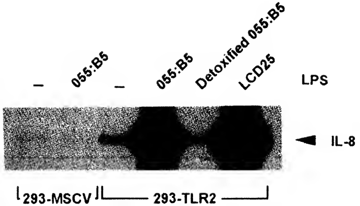

–
055:B5
–
055:B5
Detoxified 055:B5
LCD25
LPS
IL-8
293-MSCV
293-TLR2

FIG. 9

GTTATGCCTAGAAAACATTTCTCAAGAATTAGAATTACGATATGCTGTCAAACACAATGA
CTTATTTGAACCTCTTTTATTTGTAGGTTGAAGCACTGGACAATGCCACATACTTTGTGG
ATGGTGTGGGTCTTGGGGGTCATCATCAGCCTCTCCAAGGAAGAATCCTCCAATCAGGCT
TCTCTGTCTTGTGACCGCAATGGTATCTGCAAGGGCAGCTCAGGATCTTTAAACTCCATT
CCCTCAGGGCTCACAGAAGCTGTAAAAAGCCTTGACCTGTCCAACAACAGGATCACCTAC
ATTAGCAACAGTGACCTACAGAGGTGTGTGAACCTCCAGGCTCTGGTGCTGACATCCAAT
GGAATTAACACAATAGAGGAAGATTCTTTTTCTTCCCTGGGCAGTCTTGAACATTTAGAC
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TGTACCCTTAATGGAGTTGGTAATTTTAGAGCATCTGATAATGACAGAGTTATAGATCCA
GGTAAAGTGGAAACGTTAACAATCCGGAGGCTGCATATTCCAAGGTTTTACTTATTTTAT
GATCTGAGCACTTTATATTCACTTACAGAAAGAGTTAAAAGAATCACAGTAGAAAACAGT
AAAGTTTTTCTGGTTCCTTGTTTACTTTCACAACATTTAAAATCATTAGAATACTTGGAT
CTCAGTGAAAATTTGATGGTTGAAGAATACTTGAAAAATTCAGCCTGTGAGGATGCCTGG
CCCTCTCTACAAACTTTAATTTTAAGGCAAAATCATTTGGCATCATTGGAAAAAACCGGA
GAGACTTTGCTCACTCTGAAAAACTTGACTAACATTGATATCAGTAAGAATAGTTTTCAT
TCTATGCCTGAAACTTGTCAGTGGCCAGAAAAGATGAAATATTTGAACTTATCCAGCACA
CGAATACACAGTGTAACAGGCTGCATTCCCAAGACACTGGAAATTTTAGATGTTAGCAAC
AACAATCTCAATTTATTTTCTTTGAATTTGCCGCAACTCAAAGAACTTTATATTTCCAGA
AATAAGTTGATGACTCTACCAGATGCCTCCCTCTTACCCATGTTACTAGTATTGAAAATC
AGTAGGAATGCAATAACTACGTTTTCTAAGGAGCAACTTGACTCATTTCACACACTGAAG
ACTTTGGAAGCTGGTGGCAATAACTTCATTTGCTCCTGTGAATTCCTCTCCTTCACTCAG
GAGCAGCAAGCACTGGCCAAAGTCTTGATTGATTGGCCAGCAAATTACCTGTGTGACTCT
CCATCCCATGTGCGTGGCCAGCAGGTTCAGGATGTCCGCCTCTCGGTGTCGGAATGTCAC
AGGACAGCACTGGTGTCTGGCATGTGCTGTGCTCTGTTCCTGCTGATCCTGCTCACGGGG
GTCCTGTGCCACCGTTTCCATGGCCTGTGGTATATGAAAATGATGTGGGCCTGGCTCCAG
GCCAAAAGGAAGCCCAGGAAAGCTCCCAGCAGGAACATCTGCTATGATGCATTTGTTTCT
TACAGTGAGCGGGATGCCTACTGGGTGGAGAACCTTATGGTCCAGGAGCTGGAGAACTTC
AATCCCCCCTTCAAGTTGTGTCTTCATAAGCGGGACTTCATTCCTGGCAAGTGGATCATT
GACAATATCATTGACTCCATTGAAAAGAGCCACAAAACTGTCTTTGTGCTTTCTGAAAAC
TTTGTGAAGAGTGAGTGGTGCAAGTATGAACTGGACTTCTCCCATTTCCGTCTTTTTGAT
GAGAACAATGATGCTGCCATTCTCATTCTTCTGGAGCCCATTGAGAAAAAAGCCATTCCC
CAGCGCTTCTGCAAGCTGCGGAAGATAATGAACACCAAGACCTACCTGGAGTGGCCCATG
GACGAGGCTCAGCGGGAAGGATTTTGGGTAAATCTGAGAGCTGCGATAAAGTCCTAGGTT
CCCATATTTAAGACCAGTCTTTGTCTAGTTGGGATCTTTATGTCACTAGTTATAGTTAAG
TTCATTCAGACATAATTATATAAAAACTACGTGGATGTACCGTCATTTGAGGACTTGCTT
ACTAAAACTACAAAACTTCAAA

FIG. 10

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MPHTLWMVWVLGVIISLSKEESSNQASLSCDRNGICKGSSGSLNSIPSGLTEAVKSLDL
SNNRITYISNSDLQRCVNLQALVLTSNGINTIEEDSFSSLGSLEHLDLSYNYLSNLSSS
WFKPLSSLTFLNLLGNPYKTLGETSLFSHLTKLQILRVGNMDTFTKIQRKDFAGLTFLE
ELEIDASDLQSYEPKSLKSIQNVSHLILHMKQHILLLEIFVDVTSSVECLELRDTDLDT
FHFSELSTGETNSLIKKFTFRNVKITDESLFQVMKLLNQISGLLELEFDDCTLNGVGNF
RASDNDRVIDPGKVETLTIRRLHIPRFYLFYDLSTLYSLTERVKRITVENSKVFLVPCL
LSQHLKSLEYLDLSENLMVEEYLKNSACEDAWPSLQTLILRQNHLASLEKTGETLLTLK
NLTNIDISKNSFHSMPETCQWPEKMKYLNLSSTRIHSVTGCIPKTLEILDVSNNNLNLF
SLNLPQLKELYISRNKLMTLPDASLLPMLLVLKISRNAITTFSKEQLDSFHTLKTLEAG
GNNFICSCEFLSFTQEQQALAKVLIDWPANYLCDSPSHVRGQQVQDVRLSVSECHRTAL
VSGMCCALFLLILLTGVLCHRFHGLWYMKMMWAWLQAKRKPRKAPSRNICYDAFVSYSE
RDAYWVENLMVQELENFNPPFKLCLHKRDFIPGKWIIDNIIDSIEKSHKTVFVLSENFV
KSEWCKYELDFSHFRLFDENNDAAILILLEPIEKKAIPQRFCKLRKIMNTKTYLEWPMD
EAQREGFWVNLRAAIKS
```

FIG. 11

(SEQ ID NO: 1)

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Met Arg Leu Ile Arg Asn Ile Tyr Ile Phe Cys Ser Ile Val Met Thr Ala Glu Gly Asp Ala Pro Glu Leu Pro Glu Glu Arg Glu Leu
 1               5                  10                  15                  20                  25                  30

Met Thr Asn Cys Ser Asn Met Ser Leu Arg Lys Val Pro Ala Asp Leu Thr Pro Ala Thr Thr Thr Leu Asp Leu Ser Tyr Asn Leu Leu
                35                  40                  45                  50                  55                  60

Phe Gln Leu Gln Ser Ser Asp Phe His Ser Val Ser Lys Leu Arg Val Leu Ile Leu Cys His Asn Arg Ile Gln Gln Leu Asp Leu Lys
                65                  70                  75                  80                  85                  90

Thr Phe Glu Phe Asn Lys Glu Leu Arg Tyr Leu Asp Leu Ser Asn Asn Arg Leu Lys Ser Val Thr Trp Tyr Leu Leu Ala Gly Leu Arg
                95                 100                 105                 110                 115                 120

Tyr Leu Asp Leu Ser Phe Asn Asp Phe Asp Thr Met Pro Ile Cys Glu Glu Ala Gly Asn Met Ser His Leu Glu Ile Leu Gly Leu Ser
               125                 130                 135                 140                 145                 150

Gly Ala Lys Ile Gln Lys Ser Asp Phe Gln Lys Ile Ala His Leu His Leu Asn Thr Val Phe Leu Gly Phe Arg Thr Leu Pro His Tyr
               155                 160                 165                 170                 175                 180

Glu Glu Gly Ser Leu Pro Ile Leu Asn Thr Thr Lys Leu His Ile Val Leu Pro Met Asp Thr Asn Phe Trp Val Leu Leu Arg Asp Gly
               185                 190                 195                 200                 205                 210

Ile Lys Thr Ser Lys Ile Leu Glu Met Thr Asn Ile Asp Gly Lys Ser Gln Phe Val Ser Tyr Glu Met Gln Arg Asn Leu Ser Leu Glu
               215                 220                 225                 230                 235                 240

Asn Ala Lys Thr Ser Val Leu Leu Leu Asn Lys Val Asp Leu Leu Trp Asp Asp Leu Phe Leu Ile Leu Gln Phe Val Trp His Thr Ser
               245                 250                 255                 260                 265                 270
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FIG. 12A

```
Val Glu His Phe Gln Ile Arg Asn Val Thr Phe Gly Gly Lys Ala Tyr Leu Asp His Asn Ser Phe Asp Tyr Ser Asn Thr Val Met Arg
                275                 280                 285                 290                 295                 300

Thr Ile Lys Leu Glu His Val His Phe Arg Val Phe Tyr Ile Gln Gln Asp Lys Ile Tyr Leu Leu Leu Thr Lys Met Asp Ile Glu Asn
                305                 310                 315                 320                 325                 330

Leu Thr Ile Ser Asn Ala Gln Met Pro His Met Leu Phe Pro Asn Tyr Pro Thr Lys Phe Gln Tyr Leu Asn Phe Ala Asn Asn Ile Leu
                335                 340                 345                 350                 355                 360

Thr Asp Glu Leu Phe Lys Arg Thr Ile Gln Leu Pro His Leu Lys Thr Leu Ile Leu Asn Gly Asn Lys Leu Glu Thr Leu Ser Leu Val
                365                 370                 375                 380                 385                 390

Ser Cys Phe Ala Asn Asn Thr Pro Leu Glu His Leu Asp Leu Ser Gln Asn Leu Leu Gln His Lys Asn Asp Glu Asn Cys Ser Trp Pro
                395                 400                 405                 410                 415                 420

Glu Thr Val Val Asn Met Asn Leu Ser Tyr Asn Lys Leu Ser Asp Ser Val Phe Arg Cys Leu Pro Lys Ser Ile Gln Ile Leu Asp Leu
                425                 430                 435                 440                 445                 450

Asn Asn Asn Gln Ile Gln Thr Val Pro Lys Glu Thr Ile His Leu Met Ala Leu Arg Glu Leu Asn Ile Ala Phe Asn Phe Leu Thr Asp
                455                 460                 465                 470                 475                 480

Leu Pro Gly Cys Ser His Phe Ser Arg Leu Ser Val Leu Asn Ile Glu Met Asn Phe Ile Leu Ser Pro Ser Leu Asp Phe Val Gln Ser
                485                 490                 495                 500                 505                 510

Cys Gln Glu Val Lys Thr Leu Asn Ala Gly Arg Asn Pro Phe Arg Cys Thr Cys Glu Leu Lys Asn Phe Ile Gln Leu Glu Thr Tyr Ser
                515                 520                 525                 530                 535                 540
```

FIG. 12B

```
Glu Val Met Met Val Gly Trp Ser Asp Ser Tyr Thr Cys Glu Tyr Pro Leu Asn Leu Arg Gly Thr Arg Leu Lys Asp Val His Leu His
                545                 550                 555                 560                 565                 570

Glu Leu Ser Cys Asn Thr Ala Leu Leu Ile Val Thr Ile Val Val Ile Met Leu Val Leu Gly Leu Ala Val Ala Phe Cys Cys Leu His
                575                 580                 585                 590                 595                 600

Phe Asp Leu Pro Trp Tyr Leu Arg Met Leu Gly Gln Cys Thr Gln Thr Trp His Arg Val Arg Lys Thr Thr Gln Glu Gln Leu Lys Arg
                605                 610                 615                 620                 625                 630

Asn Val Arg Phe His Ala Phe Ile Ser Tyr Ser Glu His Asp Ser Leu Trp Val Lys Asn Glu Leu Ile Pro Asn Leu Glu Lys Glu Asp
                635                 640                 645                 650                 655                 660

Gly Ser Ile Leu Ile Cys Leu Tyr Glu Ser Tyr Phe Asp Pro Gly Lys Ser Ile Ser Glu Asn Ile Val Ser Phe Ile Glu Lys Ser Tyr
                665                 670                 675                 680                 685                 690

Lys Ser Ile Phe Val Leu Ser Pro Asn Phe Val Gln Asn Glu Trp Cys His Tyr Glu Phe Tyr Phe Ala His His Asn Leu Phe His Glu
                695                 700                 705                 710                 715                 720

Asn Ser Asp His Ile Ile Leu Ile Leu Leu Glu Pro Ile Pro Phe Tyr Cys Ile Pro Thr Arg Tyr His Lys Leu Lys Ala Leu Leu Glu
                725                 730                 735                 740                 745                 750

Lys Lys Ala Tyr Leu Glu Trp Pro Lys Asp Arg Arg Lys Cys Gly Leu Phe Trp Ala Asn Leu Arg Ala Ala Ile Asn Val Asn Val Leu
                755                 760                 765                 770                 775                 780

Ala Thr Arg Glu Met Tyr Glu Leu Gln Thr Phe Thr Glu Leu Asn Glu Glu Ser Arg Gly Ser Thr Ile Ser Leu Met Arg Thr Asp Cys
                785                 790                 795                 800                 805                 810

Leu
811
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FIG. 12C

(SEQ ID NO: 2)

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GAATCATCCA CGCACCTGCA GCTCTGCTGA GAGAGTGCAA GCCGTGGGGG TTTTGAGCTC ATCTTCATCA TTCATATGAG GAAATAAGTG GTAAAATCCT  100

           <MET (trans=1-s, dir=f, res+1)>
TGGAAATACA ATGAGACTCA TCAGAAACAT TTACATATTT TGTAGTATTG TTATGACAGC AGAGGGTGAT GCTCCAGAGC TGCCAGAAGA AAGGGAACTG  200

ATGACCAACT GCTCCAACAT GTCTCTAAGA AAGGTTCCCG CAGACTTGAC CCCAGCCACA ACGACACTGG ATTTATCCTA TAACCTCCTT TTTCAACTCC  300

AGAGTTCAGA TTTTCATTCT GTCTCCAAAC TGAGAGTTTT GATTCTATGC CATAACAGAA TTCAACAGCT GGATCTCAAA ACCTTTGAAT TCAACAAGGA  400

GTTAAGATAT TTAGATTTGT CTAATAACAG ACTGAAGAGT GTAACTTGGT ATTTACTGGC AGGTCTCAGG TATTTAGATC TTTCTTTTAA TGACTTTGAC  500

ACCATGCCTA TCTGTGAGGA AGCTGGCAAC ATGTCACACC TGGAAATCCT AGGTTTGAGT GGGGCAAAAA TACAAAAATC AGATTTCCAG AAAATTGCTC  600

ATCTGCATCT AAATACTGTC TTCTTAGGAT TCAGAACTCT TCCTCATTAT GAAGAAGGTA GCCTGCCCAT CTTAAACACA ACAAAACTGC ACATTGTTTT  700

ACCAATGGAC ACAAATTTCT GGGTTCTTTT GCGTGATGGA ATCAAGACTT CAAAAATATT AGAAATGACA AATATAGATG GCAAAAGCCA ATTTGTAAGT  800

TATGAAATGC AACGAAATCT TAGTTTAGAA AATGCTAAGA CATCGGTTCT ATTGCTTAAT AAAGTTGATT TACTCTGGGA CGACCTTTTC CTTATCTTAC  900

AATTTGTTTG GCATACATCA GTGGAACACT TTCAGATCCG AAATGTGACT TTTGGTGGTA AGGCTTATCT TGACCACAAT TCATTTGACT ACTCAAATAC  1000

TGTAATGAGA ACTATAAAAT TGGAGCATGT ACATTTCAGA GTGTTTTACA TTCAACAGGA TAAAATCTAT TTGCTTTTGA CCAAAATGGA CATAGAAAAC  1100

CTGACAATAT CAAATGCACA AATGCCACAC ATGCTTTTCC CGAATTATCC TACGAAATTC CAATATTTAA ATTTTGCCAA TAATATCTTA ACAGACGAGT  1200

TGTTTAAAAG AACTATCCAA CTGCCTCACT TGAAAACTCT CATTTTGAAT GGCAATAAAC TGGAGACACT TTCTTTAGTA AGTTGCTTTG CTAACAACAC  1300

ACCCTTGGAA CACTTGGATC TGAGTCAAAA TCTATTACAA CATAAAAATG ATGAAAATTG CTCATGGCCA GAAACTGTGG TCAATATGAA TCTGTCATAC  1400

AATAAATTGT CTGATTCTGT CTTCAGGTGC TTGCCCAAAA GTATTCAAAT ACTTGACCTA AATAATAACC AAATCCAAAC TGTACCTAAA GAGACTATTC  1500

ATCTGATGGC CTTACGAGAA CTAAATATTG CATTTAATTT TCTAACTGAT CTCCCTGGAT GCAGTCATTT CAGTAGACTT TCAGTTCTGA ACATTGAAAT  1600

GAACTTCATT CTCAGCCCAT CTCTGGATTT TGTTCAGAGC TGCCAGGAAG TTAAAACTCT AAATGCGGGA AGAAATCCAT TCCGGTGTAC CTGTGAATTA  1700

AAAAATTTCA TTCAGCTTGA AACATATTCA GAGGTCATGA TGGTTGGATG GTCAGATTCA TACACCTGTG AATACCCTTT AAACCTAAGG GGAACTAGGT  1800
```

FIG. 13A

TAAAAGACGT TCATCTCCAC GAATTATCTT GCAACACAGC TCTGTTGATT GTCACCATTG TGGTTATTAT GCTAGTTCTG GGGTTGGCTG TGGCCTTCTG 1900

CTGTCTCCAC TTTGATCTGC CCTGGTATCT CAGGATGCTA GGTCAATGCA CACAAACATG GCACAGGGTT AGGAAAACAA CCCAAGAACA ACTCAAGAGA 2000

AATGTCCGAT TCCACGCATT TATTTCATAC AGTGAACATG ATTCTCTGTG GGTGAAGAAT GAATTGATCC CCAATCTAGA GAAGGAAGAT GGTTCTATCT 2100

TGATTTGCCT TTATGAAAGC TACTTTGACC CTGGCAAAAG CATTAGTGAA AATATTGTAA GCTTCATTGA GAAAAGCTAT AAGTCCATCT TTGTTTTGTC 2200

TCCCAACTTT GTCCAGAATG AGTGGTGCCA TTATGAATTC TACTTTGCCC ACCACAATCT CTTCCATGAA AATTCTGATC ATATAATTCT TATCTTACTG 2300

GAACCCATTC CATTCTATTG CATTCCCACC AGGTATCATA AACTGAAAGC TCTCCTGGAA AAAAAAGCAT ACTTGGAATG GCCCAAGGAT AGGCGTAAAT 2400

GTGGGCTTTT CTGGGCAAAC CTTCGAGCTG CTATTAATGT TAATGTATTA GCCACCAGAG AAATGTATGA ACTGCAGACA TTCACAGAGT TAAATGAAGA 2500

GTCTCGAGGT TCTACAATCT CTCTGATGAG AACAGATTGT CTA $\boxed{\text{TAA}}$ AATC CCACAGTCCT TGGGAAGTTG GGGACCACAT ACACTGTTGG GATGTACATT 2600

GATACAACCT TTATGATGGC AATTTGACAA TATTTATTAA AATAAAAAAT GGTTATTCCC TTCATATCAG TTTCTAGAAG GATTTCTAAG AATGTATCCT 2700

ATAGAAACAC CTTCACAAGT TTATAAGGGC TTATGGAAAA AGGTGTTCAT CCCAGGATTG TTTATAATCA TGAAAAATGT GGCCAGGTGC AGTGGCTCAC 2800

TCTTGTAATC CCAGCACTAT GGGAGGCCAA GGTGGGTGAC CCACGAGGTC AAGAGATGGA GACCATCCTG GCCAACATGG TGAAACCCTG TCTCTACTAA 2900

AAATACAAAA ATTAGCTGGG CGTGATGGTG CACGCCTGTA GTCCCAGCTA CTTGGGAGGC TGAGGCAGGA GAATCGCTTG AACCCGGGAG GTGGCAGTTG 3000

CAGTGAGCTG AGATCGAGCC ACTGCACTCC AGCCTGGTGA CAGAGCGAGA CTCCATCTCA AAAAAAAGAA AAAAAAAAAA GAAAAAAATG GAAAACATCC 3100

TCATGGCCAC AAAATAAGGT CTAATTCAAT AAATTATAGT ACATTAATGT AATATAATAT TACATGCCAC TAAAAAGAAT AAGGTAGCTG TATATTTCCT 3200

GGTATGGAAA AAACATATTA ATATGTTATA AACTATTAGG TTGGTGCAAA ACTAATTGTG GTTTTTGCCA TTGAAATGGC ATTGAAATAA AAGTGTAAAG 3300

AAATCTATAC CAGATGTAGT AACAGTGGTT TGGGTCTGGG AGGTTGGATT ACAGGGAGCA TTTGATTTCT ATGTTGTGTA TTTCTATAAT GTTTGAATTG 3400

TTTAGAATGA ATCTGTATTT CTTTTATAAG TAGAAAAAAA ATAAAGATAG TTTTTACAGC CT 3462

FIG. 13B